

In the Claims

Please amend claims 11-14 as follows:

1. (original) A method of modeling a directed evolution protocol comprising:
applying equilibrium thermodynamics to a plurality of sequences to determine statistics of
hybridization; and
parameterizing an assembly algorithm using the statistics of hybridization.
2. (original) The method of claim 1 further comprising applying the assembly algorithm to
reassemble a plurality of sequences.
3. (original) The method of claim 2 further comprising determining crossover allocation in the
plurality of reassembled sequences.
4. (original) The method of claim 3 wherein the step of determining crossover allocation
includes estimating a fraction of the plurality of reassembled sequences containing a number of
crossovers.
5. (original) The method of claim 3 wherein the step of determining crossover allocation
includes estimating a probability that a given nucleotide position in one of the plurality of
reassembled sequences is a site of a crossover event.
6. (original) The method of claim 1 wherein the directed evolution protocol is DNA shuffling.

7. (original) The method of claim 1 wherein the directed evolution protocol is SCRATCHY.

8. (original) The method of claim 1 further comprising identifying a minimum number of required silent mutations to meet a DNA recombination objective.

9. (original) The method of claim 1 wherein the step of applying equilibrium thermodynamics to determine statistics of hybridization includes:

modeling annealing events during reassembly as a network of reactions;

determining a predicted fraction of fragments that will anneal at a given temperature;

determining a predicted distribution of annealing for overlap lengths; and

determining a portion of annealing events predicted to involve mismatches.

10. (original) The method of claim 1 wherein the assembly algorithm excludes silent crossovers.

11. (currently amended) An A method of providing an isolated nucleic acid molecule
comprising:

providing a nucleotide sequence having an amino acid sequence;

the nucleotide sequence isolated at least in part through a directed evolution experiment; and

the directed evolution experiment selected at least in part by applying equilibrium

thermodynamics to a plurality of sequences to determine statistics of hybridization and

parameterizing an assembly algorithm using the statistics of hybridization.

12. (currently amended) ~~A-The method of claim 11 wherein a vector comprising comprises~~
the nucleic acid molecule of claim 11.

13. (currently amended) ~~A-The method of claim 12 wherein a host cell containing contains~~
the vector of claim 12.

14. (currently amended) ~~A-The method of claim 11 wherein the nucleotide sequence~~
encodes a protein, encoded by the nucleic acid sequence of claim 11.

15. (original) A system for modeling a directed evolution protocol comprising:
a plurality of sequences; and
an article of software for determining statistics of hybridization of the plurality of sequences to
parameterize an assembly algorithm by applying equilibrium thermodynamics to the plurality
of sequences.